Amendments to the Specification:

Please replace the paragraph beginning at page 1, line 4 as with the following amended paragraph:

--This is a divisional of U.S. Application Serial No.09/839,479, filed April 20, 2001, which is a divisional of U.S. Application Serial No. 09/418,710, filed October 15, 1999, which is a continuation-in-part of PCT/JP98/01783, filed April 17, 1999, and claims priority from Japanese Application Nos. 9/116570, filed April 18, 1997, and 9/310027, filed October 24, 1997.--

Please replace the paragraph beginning at page 18, line 15 as with the following amended paragraph:

--Figure 1 compares the domain of BAZ (BAZ1α) with those of other proteins. In Fig. 1A, the bromodomain of BAZ (BAZ1α) is compared with that of TFIID from yeast, CCG1 from human, p300, and CBP. In Fig.1B, C4HC3 Zn finger of BAZ (BAZ1α) is compared with those of U13646, retinoblastoma binding protein RBP2, two species of MOZ, p300, and CBP. The conserved amino acids, cysteine and histidine, are indicated by "*." In both Figs. 1A and B, identical amino acids are represented by bold ~~reverse contrast~~ letters, and similar amino acids are underlined ~~represented by emphasized letters (also netted)~~. --

Please replace the paragraph beginning at page 21, line 21 as with the following amended paragraph:

--Figure 14 shows the alignments of N terminal amino acid sequences from BAZ1βS and three other members of the BAZ family. The residues with 50% or more sequence homology are indicated by bold letters ~~dark shadowed boxes~~, and those with 50% or more sequence similarity, by underlining ~~light shadowed boxes~~.--

Please replace the paragraph beginning at page 18, line 9 as with the following amended paragraph:

--Figure 1 compares the domain of BAZ (BAZ1α) with those of other proteins. In Fig. 1A, the bromodomain of BAZ (BAZ1α; SEQ ID NO:37) is compared with that of TFIID from yeast (SEQ ID NO:38), CCG1 from human (SEQ ID NO:39), ~~p300~~ PCAF (SEQ ID NO:40), and CBP (SEQ ID NO:41). In Fig.1B, C4HC3 Zn finger of BAZ (BAZ1α; SEQ ID NO:42) is compared with those of U13646 (SEQ ID NO:43), retinoblastoma binding protein RBP2 (SEQ ID NO:44), two species of MOZ (SEQ ID NOs:46 and 47, respectively), p300 (SEQ ID NO:47), and CBP (SEQ ID NO:48). The conserved amino acids, cysteine and histidine, are indicated by "*." In both Figs. 1A and B, identical amino acids are represented by reverse-contrast letters, and similar amino acids are represented by emphasized letters (also netted).--

Please replace the paragraph beginning at page 19, line 23 as with the following amended paragraph:

--Figure 6 shows alignments of the domain of BAZ2α and that of other proteins. In Fig. 6A, the bromodomain of BAZ2α (BAZ2 in the figure; SEQ ID NO:51) is aligned with BAZ (BAZ1α; SEQ ID NO:49), human CCG1 (SEQ ID NO:50), PCAF (SEQ ID NO:52), U13646 (SEQ ID NO:53) and CBP (SEQ ID NO:54). In Fig. 6B, C4HC3 Zn finger of BAZ2α (SEQ ID NO:61) is aligned with BAZ (BAZ1α; SEQ ID NO:55), U13646 (SEQ ID NO:56), retinoblastoma binding protein RBP2 (SEQ ID NO:57), 2 zinc fingers of MOZ (SEQ ID NO:58 and 60, respectively), and p300 (SEQ ID NO:60). The conserved cysteine and histidine are indicated by "*." --

Please replace the paragraph beginning at page 20, line 24 as with the following amended paragraph:

--Figure 10 compares the amino acid sequence of LH domain in BAZ2β (SEQ ID NO:65) with those of corresponding domains in other proteins (BAZ1α (SEQ ID NO:62), U13646 (SEQ ID NO:63), and BAZ2α (SEQ ID NO:64)). The positions of conserved leucine residues are indicated by arrows on the sequences. LXXLL motifs are boxed.--

Please replace the paragraph beginning at page 21, line 19 as with the following amended paragraph:

--Figure 13 shows the alignments of variable portions of BAZ1βS (SEQ ID NO:66) and BAZ1βL (SEQ ID NO:67).--

Please replace the paragraph beginning at page 21, line 21 as with the following amended paragraph:

--Figure 14 shows the alignments of N terminal amino acid sequences from BAZ1βS (SEQ ID NO:68) and three other members of the BAZ family ("BAZ1A" (SEQ ID NO:69), "BAZ2A" (SEQ ID NO:70), and "BAZ2B" (SEQ ID NO:71)). The residues with 50% or more sequence homology are indicated by dark shadowed boxes, and those with 50% or more sequence similarity, by light shadowed boxes. Conserved LXXLL motifs and C4HC3 zinc fingers are indicated on the alignments. Conserved leucine residues in the surrounding region of the LXXLL motif are indicated. The location of a bromodomain motif is indicated by a black line on the alignments.--

Please replace the paragraph beginning at page 39, line 12 as with the following amended paragraph:

--Its full-length sequence was isolated. The full-length gene for EST AA01307 was cloned as follows. First, PCR primers nb3U (SEQ ID NO:31/ TGGATGATGCTGAGGTGGATGA) and nb3L (SEQ ID NO:[~~24~~] 32/ GGGGTGCTGGATGACATCATAG) were designed to obtain a product of 184 bp specific to the primers from a testis cDNA library. The amplified product was directly purified using a QIA Quick (Qiagen) purification column. The PCR product was used as a probe to screen the testis cDNA library (Clontech HL3024a), and the cDNA clone containing the EST sequence was used to re-screen the library. This process was repeated after joining the clones. As a result, two types of nucleotide sequences were obtained and designated BAZ1β. The two sequences were further designated BAZ1βS for the shorter sequence and BAZ1βL for the longer one. The

shorter sequence consisted of 5,561 nucleotides and encoded a protein of 1527 amino acids; the longer sequence consisted of 5,573 nucleotides and encoded a protein of 1531 amino acids, containing a tandem repeat of TACAGACCCTCC (SEQ ID NO:72) in one frame. This repeat gave rise to an insertion of four amino acids LLQT at position 658, which interestingly resulted in an additional LXXLL motif. BAZ1βS had four LXXLL motifs initiated at positions 655, 658, 1000, and 1436, while BAZ1βL had five LXXLL motifs initiated at positions 655, 658, 663, 1004, and 1440. Figure 13 shows an alignment of the portions having multiple LXXLL motifs of BAZ1βS and BAZ1βL.--

Please replace the paragraph beginning at page 41, line 12 as with the following amended paragraph:

--Several motifs characteristic of transcriptional regulators were found in both BAZ1βS and BAZ1βL. They were bromodomain, C4HC3 zinc finger (C4HC3ZF), and LXXLL motifs. [~~L~~]LXXLL motifs were present in the leucine-rich domain conserved among other BAZ family member protein genes and U13646 (Fig. 9). Although the importance of this domain has not been clarified, it can form a leucine zipper responsible for forming a dimer of the protein. It has been reported that such motifs are commonly found in the transcriptional regulators of eukaryotes (Busch and Sassone-Corsi, 1990) and that LXXLL motifs also interact with the nuclear receptors (Torchia et al., (1997), Nature, 387:677-684; Heery et al., (1997), Nature 387:733-736). That the predicted amino acid sequences have extensive similarity to several kinds of transcription regulators indicates the possibility that their genes function as transcriptional regulators. This is further supported by the fact that 13 nuclear localized consensus sequences (Robbins et al., (1991), Cell, 64:615-23) were found in total based on the prediction of the cellular localization of the proteins using the PSORT program. The predicted amino acid sequences exhibited the highest similarity to BAZ1α. They also showed similarity to the proteins encoded by BAZ2α, BAZ2β, and C. elegans bromodomain gene U13646. Among the six domains, the first domain existed in BAZ2α, BAZ2β, and U13646, but not in BAZ1βS, BAZ1βL, or BAZ1α. Comparing the whole structures of these gene products, the region

between domains II and III is the most similar to that of BAZ1α (Figures 14-18). Like other members of BAZ family, these gene products also have motifs that are present in the protein assumed to be encoded by nematode (C. elegans) bromodomain gene U13646 (Wilson et al., (1994) Nature, 368:32-38) that is identified by analyzing genome sequences of the genes. Alignment of the sequences of BAZ1βS, other members of the BAZ family, and U13646 reveals that the most highly conserved regions are located between the center and the C terminus of the sequences (Figs. 14-18). For U13646, this region is not depicted in the figures, and only N terminal region is aligned with that of BAZ1βS and BAZ1α.--